



#3 OIPE

RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/10/025,648

TIME: 19:31:56

Input Set : N:\Crf3\RULE60\10025648.txt

Output Set: N:\CRF3\02142002\J025648.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Bisgard-Frantzen, Henrik
 7 Svendsen, Allan
 8 Borchert, Torben Vedel

10 (ii) TITLE OF INVENTION: AMYLASE VARIANTS

12 (iii) NUMBER OF SEQUENCES: 32

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Novo Nordisk of North America, Inc.

16 (B) STREET: 405 Lexington Avenue, Suite 6400

17 (C) CITY: New York

18 (D) STATE: New York

19 (E) COUNTRY: U.S.A.

20 (F) ZIP: 10174-6401

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/10/025,648

C--> 30 (B) FILING DATE: 19-Dec-2001

36 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 08/600,656

35 (B) FILING DATE: 13-FEB-1996

38 (viii) ATTORNEY/AGENT INFORMATION:

39 (A) NAME: Lambiris, Elias J.

40 (B) REGISTRATION NUMBER: 33,728

41 (C) REFERENCE/DOCKET NUMBER: 4318.204-US

43 (ix) TELECOMMUNICATION INFORMATION:

44 (A) TELEPHONE: 212 867 0123

45 (B) TELEFAX: 212 867 0298

48 (2) INFORMATION FOR SEQ ID NO: 1:

50 (i) SEQUENCE CHARACTERISTICS:

51 (A) LENGTH: 485 amino acids

52 (B) TYPE: amino acid

53 (C) STRANDEDNESS: single

54 (D) TOPOLOGY: linear

56 (ii) MOLECULE TYPE: peptide

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr

61 1 5 10 15

ENTERED

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```

63   Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
64           20                      25                      30
66   Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
67           35                      40                      45
69   Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
70           50                      55                      60
72   Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
73           65                      70                      75                      80
75   Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
76           85                      90                      95
78   Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
79           100                     105                     110
81   Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
82           115                     120                     125
84   Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
85           130                     135                     140
87   Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
88           145                     150                     155                     160
90   His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
91           165                     170                     175
93   Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
94           180                     185                     190
96   Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
97           195                     200                     205
99   Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
100          210                     215                     220
102   Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
103          225                     230                     235                     240
105   Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
106          245                     250                     255
108   Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
109          260                     265                     270
111   Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
112          275                     280                     285
114   Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
115          290                     295                     300
117   Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
118          305                     310                     315                     320
120   His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
121          325                     330                     335
123   Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
124          340                     345                     350
126   Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
127          355                     360                     365
129   Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
130          370                     375                     380
132   Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
133          385                     390                     395                     400
135   Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu

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Input Set : N:\Crif3\RULE60\10025648.txt

Output Set: N:\CRF3\02142002\J025648.raw

```

136          405          410          415
138 Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
139          420          425          430
141 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
142          435          440          445
144 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
145          450          455          460
147 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
148 465          470          475          480
150 Val Trp Val Lys Gln
151          485
154 (2) INFORMATION FOR SEQ ID NO: 2:
156 (i) SEQUENCE CHARACTERISTICS:
157 (A) LENGTH: 485 amino acids
158 (B) TYPE: amino acid
159 (C) STRANDEDNESS: single
160 (D) TOPOLOGY: linear
162 (ii) MOLECULE TYPE: peptide
164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
166 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp His
167 1 5 10 15
169 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ser
170 20 25 30
172 Asn Leu Arg Asn Arg Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Trp
173 35 40 45
175 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
176 50 55 60
178 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
179 65 70 75 80
181 Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
182 85 90 95
184 Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
185 100 105 110
187 Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
188 115 120 125
190 Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
191 130 135 140
193 Phe Pro Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp Arg Trp Tyr
194 145 150 155 160
196 His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
197 165 170 175
199 Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
200 180 185 190
202 Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
203 195 200 205
205 Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
206 210 215 220
208 Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
209 225 230 235 240

```

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```

211   Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
212                                245                                250                                255
214   Thr Gly Lys Glu Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
215                                260                                265                                270
217   Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
218                                275                                280                                285
220   Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
221                                290                                295                                300
223   Gly Asn Tyr Asp Met Ala Lys Leu Leu Asn Gly Thr Val Val Gln Lys
224   305                                310                                315                                320
226   His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
227                                325                                330                                335
229   Gly Glu Ser Leu Glu Ser Phe Val Gln Glu Trp Phe Lys Pro Leu Ala
230                                340                                345                                350
232   Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
233                                355                                360                                365
235   Gly Asp Tyr Tyr Gly Ile Pro Thr His Ser Val Pro Ala Met Lys Ala
236                                370                                375                                380
238   Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Asn Phe Ala Tyr Gly Thr
239   385                                390                                395                                400
241   Gln His Asp Tyr Phe Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
242                                405                                410                                415
244   Gly Asn Thr Thr His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
245                                420                                425                                430
247   Gly Pro Gly Gly Glu Lys Trp Met Tyr Val Gly Gln Asn Lys Ala Gly
248                                435                                440                                445
250   Gln Val Trp His Asp Ile Thr Gly Asn Lys Pro Gly Thr Val Thr Ile
251   450                                455                                460
253   Asn Ala Asp Gly Trp Ala Asn Phe Ser Val Asn Gly Gly Ser Val Ser
254   465                                470                                475                                480
256   Ile Trp Val Lys Arg
257                                485

```

260 (2) INFORMATION FOR SEQ ID NO: 3:

262 (i) SEQUENCE CHARACTERISTICS:

263 (A) LENGTH: 514 amino acids

264 (B) TYPE: amino acid

265 (C) STRANDEDNESS: single

266 (D) TOPOLOGY: linear

268 (ii) MOLECULE TYPE: peptide

270 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

272   Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
273   1                                5                                10                                15
275   Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
276                                20                                25                                30
278   Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
279                                35                                40                                45
281   Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
282   50                                55                                60
284   Leu Gly Glu Phe Asn Gln Lys Gly Ala Val Arg Thr Lys Tyr Gly Thr

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285	65	70	75	80
287	Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met			
288		85	90	95
290	Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly			
291		100	105	110
293	Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln			
294		115	120	125
296	Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe			
297		130	135	140
299	Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His			
300		145	150	155
302	Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr			
303		165	170	175
305	Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu			
306		180	185	190
308	Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His			
309		195	200	205
311	Pro Glu Val Val Thr Glu Leu Lys Ser Trp Gly Lys Trp Tyr Val Asn			
312		210	215	220
314	Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys			
315		225	230	235
317	Phe Ser Phe Phe Pro Asp Trp Leu Ser Asp Val Arg Ser Gln Thr Gly			
318		245	250	255
320	Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys			
321		260	265	270
323	Leu His Asn Tyr Ile Met Lys Thr Asn Gly Thr Met Ser Leu Phe Asp			
324		275	280	285
326	Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Thr			
327		290	295	300
329	Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro			
330		305	310	315
332	Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln			
333		325	330	335
335	Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala			
336		340	345	350
338	Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp			
339		355	360	365
341	Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile			
342		370	375	380
344	Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His			
345		385	390	395
347	Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Val			
348		405	410	415
350	Thr Glu Lys Pro Gly Ser Gly Leu Ala Leu Ile Thr Asp Gly Pro			
351		420	425	430
353	Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val			
354		435	440	445
356	Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser			
357		450	455	460

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/025,648

DATE: 02/14/2002

TIME: 19:31:58

Input Set : N:\Crf3\RULE60\10025648.txt

Output Set: N:\CRF3\02142002\J025648.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]